

[illegible]

Fig. 1

	34	43	39	42	48	31	25	26	28	30																																	
hApo2LI	D	C	A	G	D	-	-	F	H	K	K	I	G	L	F	C	C	R	G	C	P	A	G	H	Y	L	K	A	P	C	T	E	P	C	G	N	S	T	C	L			
hTNFR1	V	C	P	Q	G	K	-	-	Y	I	H	P	Q	N	S	I	C	C	T	K	C	H	K	G	T	Y	L	Y	N	D	C	P	G	P	G	Q	D	T	D	C	R		
hTNFR2	T	C	R	L	R	E	-	-	Y	Y	D	Q	T	A	Q	M	C	C	S	K	C	S	P	G	Q	H	A	K	V	F	C	T	K	T	-	S	D	T	V	C	D		
hTNFRip	T	C	R	D	Q	E	K	E	-	Y	Y	E	P	Q	H	R	I	C	C	S	R	C	P	P	G	T	Y	V	S	A	K	C	S	R	I	-	R	D	T	V	C	A	
hFAS/Apo1	N	L	E	G	L	-	-	-	H	H	D	G	Q	F	C	H	K	P	C	P	P	G	E	R	K	A	R	D	C	T	V	N	G	D	E	P	D	C	V	-			
hLINGR	A	C	P	T	G	-	-	-	L	Y	T	H	S	G	E	C	K	A	C	N	L	G	E	G	V	A	Q	P	C	G	A	-	-	N	Q	T	V	C	E	-			
hCD40	A	C	R	E	K	-	-	-	Q	Y	L	I	N	S	Q	C	C	S	L	C	Q	P	G	Q	K	L	V	S	D	C	T	E	F	-	T	E	T	E	C	L	-		
hCD27	S	C	P	E	R	-	-	-	H	Y	W	A	Q	G	K	L	C	C	Q	M	C	E	P	G	T	F	L	V	K	D	C	D	Q	H	R	K	A	A	Q	C	D		
hCD30	T	C	H	G	N	P	S	H	-	Y	Y	D	K	A	V	R	R	C	C	Y	R	C	P	M	G	L	F	P	T	Q	Q	C	P	Q	R	-	-	P	T	D	C	R	K
hOX40	H	C	V	G	D	T	-	-	-	Y	P	S	N	D	R	C	C	H	E	C	R	P	P	G	N	G	M	V	S	R	C	S	R	S	-	Q	N	T	V	C	R	-	

hApo2LI	72	V	C	P	Q	D	-	T	F	L	A	W	E	N	H	H	S	E	C	A	R	C	-	Q	A	C	D	E	Q	A	S	Q	V	A	L	E	N	C	S	A	V	A	D	T	R	C	G
hTNFR1	83	E	C	E	S	G	-	S	F	T	A	S	E	N	H	L	R	H	C	L	S	C	-	S	K	C	R	K	E	M	G	Q	V	E	I	S	S	C	T	V	D	R	D	T	V	C	G
hTNFR2	77	S	C	E	D	S	T	Y	T	Q	L	W	N	W	V	-	P	E	C	L	S	C	G	S	R	C	S	S	-	-	D	Q	V	E	T	Q	A	C	T	R	E	Q	N	R	I	C	T
hTNFRip	82	T	C	A	E	N	S	Y	N	E	H	W	N	Y	L	-	T	I	C	Q	L	C	-	R	P	C	D	P	V	M	G	L	E	E	I	A	P	C	T	S	K	R	K	T	Q	C	R
hFAS/Apo1	84	P	C	Q	E	G	K	E	Y	T	D	K	A	H	F	S	S	K	C	R	R	C	-	R	L	C	D	E	G	H	G	L	E	V	E	I	N	C	T	R	T	Q	N	T	K	C	R
hLINGER	66	P	C	L	D	S	V	T	F	S	D	V	V	S	A	T	E	P	C	K	P	C	-	T	E	C	V	G	L	-	-	Q	S	M	S	A	P	C	V	E	A	D	D	A	V	C	R
hCD40	61	P	C	G	E	S	E	F	L	D	T	W	N	R	E	-	T	H	C	H	Q	H	-	K	Y	C	D	P	N	L	G	L	R	V	Q	Q	K	G	T	S	E	T	D	I	C	T	
hCD27	64	P	C	I	P	G	V	S	F	S	P	D	H	H	T	R	P	H	C	E	S	C	-	R	H	C	N	S	G	L	L	V	R	-	-	N	C	T	I	T	A	N	A	E	C	A	
hCD30	68	Q	C	E	P	D	-	Y	Y	L	D	E	A	D	R	-	-	C	T	A	C	-	V	T	C	S	R	D	D	L	V	E	K	T	-	P	C	A	W	N	S	S	R	V	C		
hOX40	66	P	C	G	P	G	-	F	Y	N	D	V	V	S	S	K	P	-	C	K	P	C	-	T	W	C	N	L	R	S	G	S	E	R	K	Q	L	C	T	A	T	Q	D	T	V	C	

FIG. 2A

116 127 120 126 129 109 105 106 108 109
 hApo2LI hTNFR1 hTNFR2 hTNFRrp hFAS/Apo1 hLINGFR hCD40 hCD27 hCD30 hOX40

CKPGWFVEQVSQCVS SPFYCQPCLDGGA LHRHTRLLCSRRD - TDCG - T
 CRKNQYRHYWSENL - - - FQCFNCSLCLNG - - TVHLSCQEKQNTVCG - - T
 CRPGWYCALSKQEGC - - - RLCAPLRKC RP G - FGVARPGTETSDVVCCK - P
 CQPGMFCAAWALEC - - - THCELLSDC PPGTEAELKDEVGKGNHCV - P
 CKPNFF - - CNSTVC - - - EHC DPCTKCEHGI - - - IKECTLTSTNTKCK -
 CAYGYQDETT - - - GRCEACRVCEAGSGL - VFSCQDKQNTVCE - E
 CEEGWHCTSEAC - - - ESCVLHRS CSPGFG - VKQIATGVSDTICE - P
 CRNGWQCRDKEC - - - TECDPLPNPSLTARSSQALSPHPQPT HLP -
 - CRPGMFCSTSAVNSC - - - ARCFFHSVCPAGMIVKFPGTAQK - NTVCE -
 - CRA GTQPLDSYKPG - - - VDCA - - - - - - - - - - - - - - -

164 168 164 170 149 146 127
 hApo2LI hTNFR1 hTNFR2 hTNFRrp hLINGFR hCD40 hOX40
 CLPGFYEHGD - - - GCVSCPT
 CHAGFFLREN - - - ECVSCSNCKK - - - SLECTK - - - LCL
 CAPGTFSTNTSSSTDICRPHQICNVVAIPGNASM - - - DAVCT
 CKA GHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTCK
 CPDGTYSDEANHVDPCLPCTVCE DTERQLRECTRW - ADAECE
 CPVGFFSNVSSAFEEKCHPWTSCETKDLVVQQAGTNKTDVVVCG
 PCPPGHFSPGD - - NQACKPWTNCTLAGKHTLQPASNSSDAICE

FIG. 2B

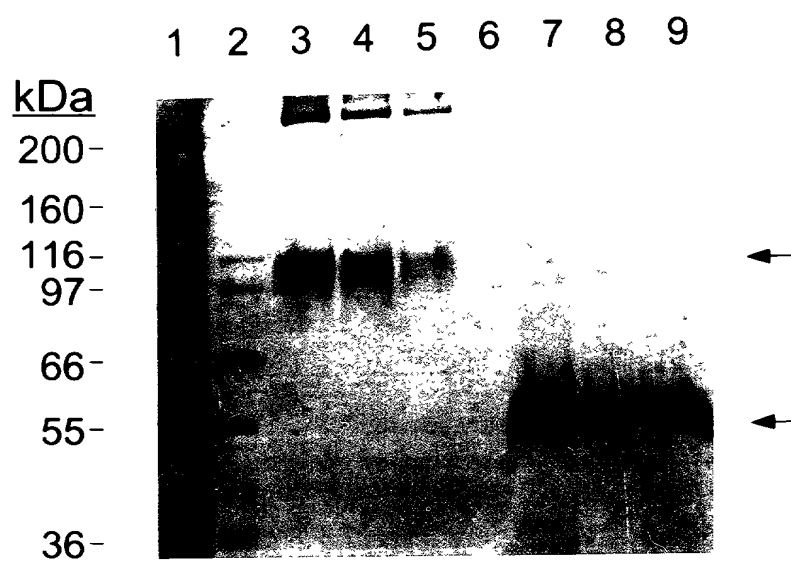


FIG. 3

541 ACGGCTACTC TGTTCCCGCA GAGATACTGA CTGTGGGACC TGCCCTGCCCTG GCTTCTATGA
152 R L L C S R R D T D C G T C L P G F Y E

601 ACATGGCGAT GGCTGCGTGT CCTGCCCCAC GAGCACCCCTG GGGAGCTGTC CAGAGCGCTG
172 H G D G C V S C P T S T L G S C P E R C

661 TGCCGCTGTC TGTGGCTGGA GGCAGATGTT CTGGGTCCAG GTGCTCCTGG CTGGCCTTGT
192 A A V C G W R Q M F W V Q Y L L A G L Y

721 GGTCCCCCTC CTGCTTGGGG CCACCCCTGAC CTACACATAC CGCCACTGCT GGCCTCACAA
212 V P L L L G A T L T Y T Y R H C W P H K

781 GCCCCTGGTT ACTGCAGATG AAGCTGGGAT GGAGGCTCTG ACCCCACCAC CGGCCACCCA
232 P L V T A D E A G M E A L T P P P A T H

841 TCTGTACCCC TTGGACAGCG CCCACACCCT TCTAGCACCT CCTGACAGCA GTGAGAAGAT
252 L S P L D S A H T L L A P P D S S E K I

901 CTGCACCGTC CAGTTGGTGG GTAACAGCTG GACCCCTGGC TACCCCGAGA CCCAGGAGGC
272 C T V Q L V G N S W T P G Y P E T Q E A

961 GCTCTGCCCG CAGGTGACAT GGTCTGGGA CCAGTTGCCC AGCAGAGCTC TTGGCCCCCG
292 L C P Q V T W S W D Q L P S R A L G P A

1021 TGCTGCGCCC ACACTCTCGC CAGAGTCCCC AGCCGGCTCG CCAGCCATGA TGCTGCAGCC
312 A A P T L S P E S P A G S P A M M L Q P

FIG. 4B

1081 GGGCCCGCAG CTCTACGACG TGATGGACGC GGTCCCAGCG CGGCGCTGGA AGGAGTTCGT
332 G P Q L Y D V M D A V P A R R W K E F V

1141 GCGCAGCGTG GGGCTGCGG AGGCAGAGAT CGAAGCCGTG GAGGTGGAGA TCGGCCGCTT
352 R T L G L R E A E I E A V E V E I G R F

1201 CCGAGACCAG CAGTACGAGA TGCTCAAGCG CTGGCGCCAG CAGCAGCCCG CGGGCCTCGG
372 R D Q Q Y E M L K R W R Q Q Q P A G L G

1261 AGCCGTTTAC GCGGCCCTGG AGCGCATGGG GCTGGACGGC TGC GTGGAAG ACTTGCCGAG
392 A V Y A A L E R M G L D G C V E D L R S

1321 CCGCCTGCAG CGCGGCCCGT GACACGGCGC CCACTTGCCA CCTAGGCGCT CTGGTGGCCC
412 R L Q R G P

1381 TTGCAGAAGC CCTAAGTACG GTTACTTATG CGGTAGACA TTTTATGTCA CTTATTAGC

1441 CGCTGGCAGG GCCCTGGTA GCAGCACCAG CCGGCCCCAC CCTGCTCGC CCTATCGCT

1501 CCAGCCAAGG CGAAGAAGCA CGAACGAATG TCGAGAGGGG GTGAAGACAT TTCTCAACTT

1561 CTCGGCCGGA GTTTGGCTGA GATCGCGGTA TTAAATCTGT GAAAGAAAC AAAAAAAAAA

1621 AAAAAAAAAA AAAA

FIG. 4C

Apo3	1	MEQRP	RGCA	VA	AA	LL	VL	LL	GARA	QG	TR	SP	RR	----
TNFR1	1	MGLST	VPDL	LL	PL	-	VLL	ELL	VGI	PS	GV	IG	LV	PH
Fas/Apo1	1	MLGI	WTLL	PL	VL	TS	VA	RL	SS	KS	VNA	QV	TD	INS
														KG
														LE
														LR
														KT
														VT
														TV
Apo3	33	CD	CAGD	FF	KK	IG	GL	CC	RG	CP	AG	HY	LK	AP
TNFR1	44	CP	QG	KY	IH	PQ	NN	SI	CC	TK	CH	KG	TY	LN
Fas/Apo1	45	ET	QN	LE	GL	HD	GQ	FF	CH	KP	CP	PP	GE	KA
														RD
														CV
														P
Apo3	73	CP	QD	TF	LA	WE	NH	HN	SE	CA	RC	QA	CD	EQ
TNFR1	85	CE	SG	SF	TA	SE	NH	LR	H-	CL	SC	SK	CR	KE
Fas/Apo1	85	CQ	EG	KE	YT	DK	AH	FS	SK	CR	RC	RL	CD	EG
														GH
														GL
														VE
														IN
														CT
														RT
														QN
														TK
														CR
Apo3	117	CK	PG	WF	VE	CQ	VS	Q	CV	SS	SP	FY	CQ	PC
TNFR1	127	CR	KN	QY	RH	YS	EN	LF	Q	-	-	-	-	CF
Fas/Apo1	129	CK	PN	FF	-	-	CN	ST	VC	EH	-	-	-	CD
														PC
														TK
														CC
														EH
														GI
														IK
														EE
														CT
														TL
														TS
														N
														TK
														CK
														KE
Apo3	165	CL												

FIG. 5

Apo3	338	VMDA	VPA	RR	WK	FF	VR	TL	GL	REA	EE	IE	AV	VE	IG	-	-	FR	QQ	YE
TNFR1	333	VVEN	VPP	LR	WK	FF	VR	RL	GL	SD	HE	ID	RL	EL	QG	-	-	CL	RE	AQ
Fas/Apo1	220	IAGV	MT	LS	VK	GF	VR	KN	GV	NE	AK	ID	IE	IK	ND	VQ	DT	AE	QK	VQ
FADD	104	ICDN	VGK	-	D	WR	RL	AR	QL	KV	SD	TK	ID	SE	DR	YP	RN	-	LT	ER
TRADD	211	NRPL	SLK	-	DQ	TF	AR	SV	GL	KW	RR	KV	GR	-	SL	QR	GC	RA	LR	DP
RIP	291	IREN	LGK	-	HW	KN	CA	RR	KL	GF	TQ	SA	ID	IE	DH	DY	ER	DG	LE	KV
Reaper	1					MA	VA	FY	IP	DQ	AT	LL	RE	AE	QK	EE	QI	IL	-	LR

Apo3	378	MLKRWRRQQP--	AGLGAVYA	ALERMGL	-DGC	VEDLRS
TNFR1	374	MLATWRRRT	PPRREA	TLLEL	GRVLL	RDMDL-LGCCLEEDIEE
Fas/Apo1	261	LLRNWHQLHG	-KKEAYDTL	IKDL	LKKANL	CTLA-EKIQ
FADD	144	SLRIWKNT	E-KEN	ATVAHL	VGALL	RSC--QMNLVADLV
TRADD	251	SLAYEYER	EGLYEQ	AFQL	LLRRFV	-QAEGRRATLQRLVE
RIP	332	MLQKWMREG	IKGA	TVGKL	AAQL	HQC--SRIDLSSLT
Reaper	34	FLATVVL	ETLKQY	TSCH	PKTGR	KSGKYRKP

6
6
F

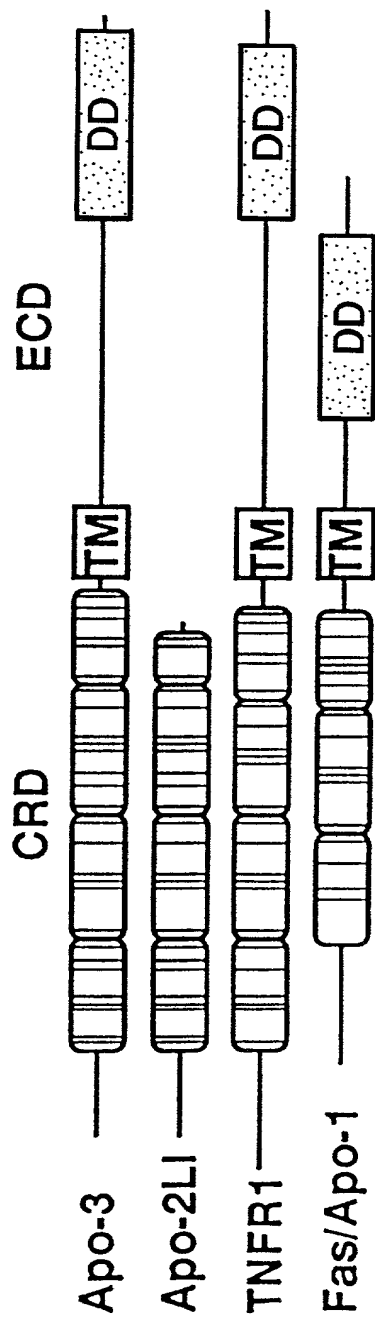


FIG. 7

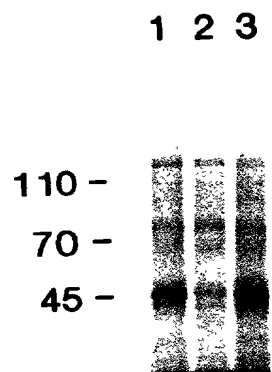


FIG. 8

1 2 3 4 5 6 7 8 9

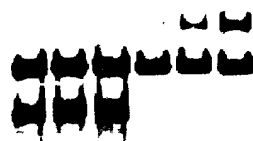


FIG. 10

FIG. 9A

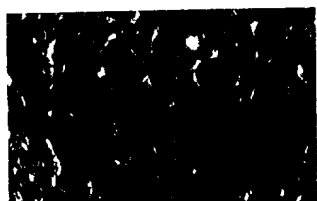


FIG. 9B



FIG. 9C

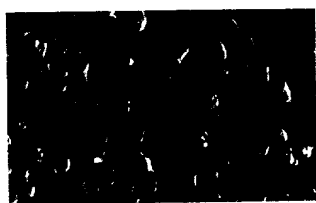


FIG. 9D



FIG. 9E

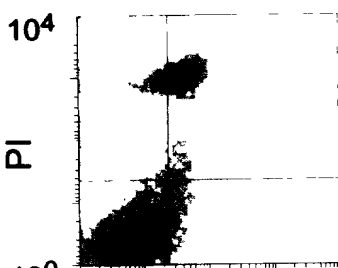


FIG. 9F

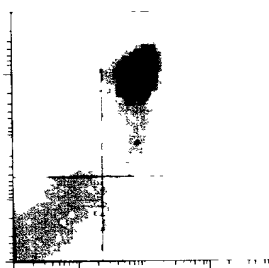


FIG. 9G

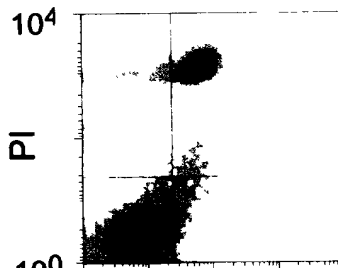


FIG. 9H

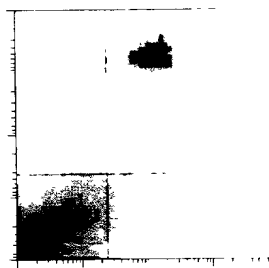


FIG. 9I

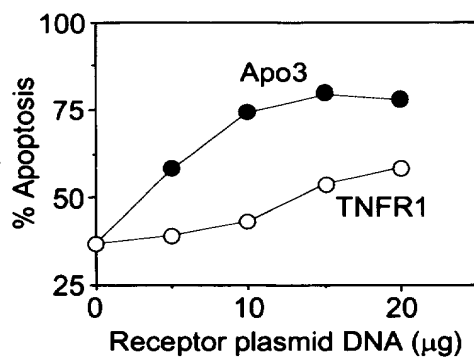


FIG. 9J



Transfection

pRK5
TNFR1
Apo-3

◀ **Phospho-C-Jun**

FIG. 11

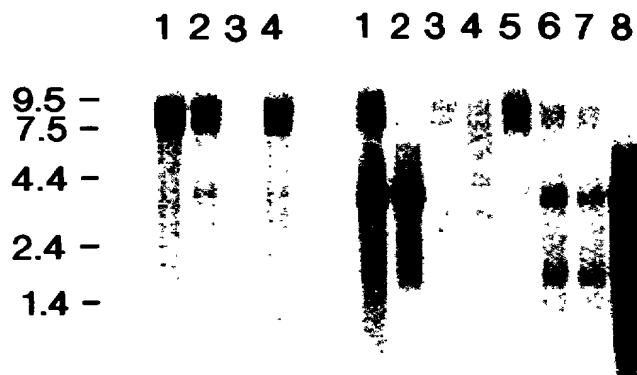


FIG. 12